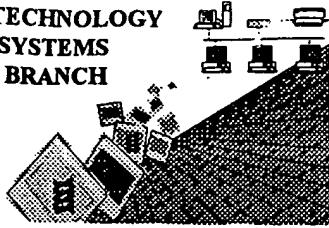


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

RECEIVED

Application Serial Number:

09/831,253C

OCT 21 2003

Source:

16pp

Date Processed by STIC:

10/7/2003

TECH CENTER 1000/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE).
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised: 10/08/2003

Raw Sequence Listing Error Summary

| <u>ERROR DETECTED</u> | <u>SUGGESTED CORRECTION</u> | <u>SERIAL NUMBER:</u> <u>09/831,283C</u> |
|---|--|--|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." | |
| 2 <input type="checkbox"/> Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 <input checked="" type="checkbox"/> Misaligned Amino Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. | |
| 4 <input type="checkbox"/> Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text . | |
| 5 <input type="checkbox"/> Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. | |
| 6 <input type="checkbox"/> PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 7 <input type="checkbox"/> Skipped Sequences (OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped | |
| 8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES) | Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) <u>166</u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000 | |
| 9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 10 <input type="checkbox"/> Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence | |
| 11 <input type="checkbox"/> Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) | |
| 12 <input type="checkbox"/> PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 <input type="checkbox"/> Misuse of n/Xaa | "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u> | |



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,253C

DATE: 10/07/2003
TIME: 10:20:47

Input Set : A:\0134469 sequence listing .txt
Output Set: N:\CRF4\10072003\I831253C.raw

1 <110> APPLICANT: EZQUERRO SAENZ, Ignacio Jose
2 LASARTE SAGASTIBELZA, Juan Jose
3 PRIETO VALTUEYA, Jesus
4 BORRAS CUESTA, Francisco
6 <120> TITLE OF INVENTION: TGFbb1-inhibitor peptides
8 <130> FILE REFERENCE: U-013446-9
10 <140> CURRENT APPLICATION NUMBER: 09/831,253C
11 <141> CURRENT FILING DATE: 2001-06-27
13 <150> PRIOR APPLICATION NUMBER: PCT/ES99/00375
14 <151> PRIOR FILING DATE: 1999-11-23
16 <150> PRIOR APPLICATION NUMBER: P9802465
17 <151> PRIOR FILING DATE: 1998-11-24
E--> 19 <160> NUMBER OF SEQ ID NOS: 160 > 179

Suggestion: PLEASE
consult
Sequence
Rules
for
Does Not Comply
Corrected Diskette Needed
VALID

IMPORTANT: see p.3
(total number
of Sequences
is 178)

ERRORED SEQUENCES

do NOT use alphabetical headings

Replace with <160>

E--> 22 <210> SEQ ID NO: ~~SEQ ID NO: 1~~ In new Sequence Rules
23 <211> LENGTH: 15 ~~delete~~ format. CRF software inserts
E--> 24 <212> TYPE: Peptide PRT alphabetical headings.
25 <213> ORGANISM: Artificial sequence
W--> 26 <220> FEATURE: Domain NEVER insert a response to <220>
W--> 26 <220> FEATURE: Domain <2217> insert <2217> and move response to <2217> line.
W--> 27 <223> OTHER INFORMATION: Derived from human TGBb1 position 319-333
W--> 28 <400> ~~SEQUENCE: His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu~~ do not
29 <400> ~~1~~ 5 10 15 15 insert this
E--> 32 <210> SEQ ID NO: ~~SEQ ID NO: 2~~ on <400>
33 <211> LENGTH: 14 ~~delete~~ misaligned nos. See item 3 on Enviro
E--> 34 <212> TYPE: Peptide PRT summary
35 <213> ORGANISM: Artificial sequence sheet
W--> 36 <220> FEATURE: Domain <2217> Move this
W--> 36 <220> FEATURE: Domain <2217> under <400> line
37 <223> OTHER INFORMATION: Derived from human TGBb1 position 322-335
W--> 38 <400> ~~SEQUENCE: Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr~~
39 <400> ~~2~~ 5 10 10 move
E--> 43 <210> SEQ ID NO: ~~SEQ ID NO: 3~~ under <400> line
44 <211> LENGTH: 12
E--> 45 <212> TYPE: Peptide
46 <213> ORGANISM: Artificial sequence
W--> 47 <220> FEATURE: Domain
W--> 47 <220> FEATURE: Domain <2217>
48 <223> OTHER INFORMATION: Derived from rat TGBb1 type III receptor position 731-742
W--> 49 <400> ~~SEQUENCE: Thr Ser Leu Asp Ala Thr Met Ile Trp Thr Met Met~~
<400> ~~3~~ 5 10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,253C

DATE: 10/07/2003

TIME: 10:20:47

Input Set : A:\0134469 sequence listing .txt

Output Set: N:\CRF4\10072003\I831253C.raw

50 5 10
E--> 53 <210> SEQ ID NO: SEQ ID NO: 4
54 <211> LENGTH: 15
E--> 55 <212> TYPE: Peptide *Same error*
56 <213> ORGANISM: Artificial sequence
W--> 57 <220> FEATURE: Domain
W--> 57 <220> FEATURE: Domain
58 <223> OTHER INFORMATION: Derived from rat TGBb1 position 245-259
W--> 59 <400> SEQUENCE: Ser Asn Pro Tyr Ser Ala Phe Gln Val Asp Ile Ile Val Asp Ile
60 5 10 15
E--> 63 <210> SEQ ID NO: SEQ ID NO: 5 *same error*
64 <211> LENGTH: 9
E--> 65 <212> TYPE: Peptide *invalid response.*
66 <213> ORGANISM: Synthetic peptide derived from P54
W--> 67 <220> FEATURE: Domain *See item 10 on Error*
W--> 67 <220> FEATURE: Domain
W--> 68 <400> SEQUENCE: Thr Ser Leu Met Ile Trp Thr Met Met
69 5
E--> 72 <210> SEQ ID NO: SEQ ID NO: 6 *Same*
73 <211> LENGTH: 14
E--> 74 <212> TYPE: Peptide *Same*
75 <213> ORGANISM: Synthetic peptide from human TGBb1 type III receptor
W--> 76 <220> FEATURE: Domain: 729-742
W--> 76 <220> FEATURE: Domain: 729-742
W--> 77 <400> SEQUENCE: Thr Ser Leu Asp Ala Ser Ile Ile Trp Ala Met Met Gln Asn
78 5 10
E--> 81 <210> SEQ ID NO: SEQ ID NO: 7 *Same*
82 <211> LENGTH: 14
E--> 83 <212> TYPE: Peptide *Same*
84 <213> ORGANISM: Synthetic peptide from human TGBb1 type III receptor
W--> 85 <220> FEATURE: Domain: 241-254
W--> 85 <220> FEATURE: Domain: 241-254
W--> 86 <400> SEQUENCE: Ser Asn Pro Tyr Ser Ala Phe Gln Val Asp Ile Thr Ile Asp
87 5 10
E--> 90 <210> SEQ ID NO: SEQ ID NO: 8 *Same*
91 <211> LENGTH: 15
E--> 92 <212> TYPE: Peptide *Same*
93 <213> ORGANISM: Synthetic peptide from pig endoglin
W--> 94 <220> FEATURE: Domain: 247-261
W--> 94 <220> FEATURE: Domain: 247-261
W--> 95 <400> SEQUENCE: Glu Ala Val Leu Ile Leu Gln Gly Pro Pro Tyr Val Ser Trp Leu
96 5 10 15
E--> 99 <210> SEQ ID NO: SEQ ID NO: 9 *Same*
100 <211> LENGTH: 15
E--> 101 <212> TYPE: Peptide *Same*
102 <213> ORGANISM: Synthetic peptide from pig endoglin
W--> 103 <220> FEATURE: Domain: 445-459
W--> 103 <220> FEATURE: Domain: 445-459
W--> 104 <400> SEQUENCE: Leu Asp Ser Leu Ser Phe Gln Leu Gly Leu Tyr Leu Ser Pro His

09/83/253c 3

<210> SEQ ID NO: 132
<211> 15 *same errors*
<212> Peptide
<213> Synthetic peptide from rat TGBb1 type III receptor
<220> Domain: 350-364
<223> ~~Descripcion/Posicion~~ delete
<400> Val Ala Asn Arg Phe His Leu Arg Leu Glu Asn Asn Glu Glu Met
5 10 15

09/83, 253c 4

<210> SEQ ID NO: 165
<211> 12
<212> Peptide
<213> Synthetic peptide from human alpha 2 microglobulin
<220> Domain: 554-565
<400> Asp Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala

Sequence 166 missing. If intentionally skipped, please use
format shown
in item 8 of
Error summary
sheet

<210> SEQ ID NO: 167

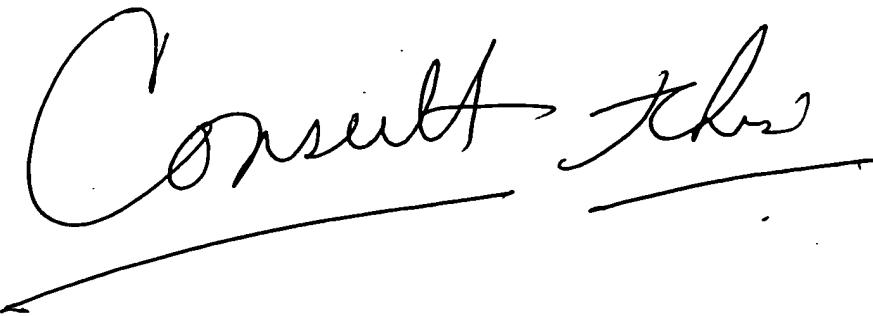
The types of errors shown exist throughout
the Sequence Listing. Please check all
sequences for similar errors.

Every sequence in submitted file is
erred.

Please consult sample Sequence Listing
(attached)

<110> Smith, John; Smithgene Inc.
 <120> Example of a Sequence Listing
 <130> 01-00001
 <140> PCT/EP98/00001
 <141> 1998-12-31
 <150> US 08/999,999
 <151> 1997-10-15
 <160>
 <170> PatentIn version 2.0
 <210> 1
 <211> 389
 <212> DNA
 <213> Paramecium sp.
 <220>
 <221> CDS
 <222> (279)...(389)
 <300>
 <301> Doc. Richard
 <302> Isolation and Characterization of a Gene Encoding a
 Protease from Paramecium sp.
 <303> Journal of Genes
 <304> 1
 <305> 4
 <306> 1-7
 <307> 1988-06-31
 <308> 123456
 <309> 1988-06-31

 <400> 1 agctcgatgc atttccctgtgt ccccttcctt ctggggcttc caccctcgta atcagatccc 60
 agggagatcg tcttgaccctt cctctgcctt tgcagcttca caggcaggca ggccaggcagc E 120
 tcatgtggca attgtctggca gtgtccacagg cttttcagcc aggcttaggg tgggtttccgc 180
 cgcggcgccgg cggccccctt cgcgttcctt tgcgccttc ctttcgtctt ccttcgtctc 240

Consult this


Appendix 3, page 2.

ggacacctgatt aggtgagcag gaggagggggg cagtttgc atg gtt tca atg ttc agc 296
 Met Val Ser Met Phe Ser 1

tgc tct ttc aaa tgg cct gga ttt tgt ttg tct gtt tgt ttg ttc caa 344
 Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Cln 10 15 20

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
 Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Cln Pro Asn 23 30 35

<210> 2

<211> 37

<212> PRT

<213> Paramecium sp.

<<00> 2
 Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu 1 10 15

Phe Val Cys Leu Phe Cln Cys Pro Lys Val Leu Pro Cys His Ser Ser 20 25 30

Leu Cln Pro Asn Leu 35

<210>

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3
 Met Val Asn Leu Glu Pro Met His Thr Glu Ile 1 10

<210> 4

<400> 4

000

[Annex VIII follows]